Figure 1:

ORF of Isocitrate dehydrogenase 1 (XM_055088)

(nucleic acid sequence: SEQ ID NO:1; amino acid sequence: SEQ ID NO:2)

```
  5   1     GGC GGC GAA GCG GGG GCA CGC CCT CGC ACA CGC AGA GAT AAA TTG    45
      46    TGC TCC CAT GAC CTT TAT TTG GAA AGT GCC TGC GGG CCT AAA ATT    90
      91    GGC CTT TGT CCC ACC GAG TAC ACT CAG CAC TGT ACT TTA AAC CGG    135
      136   ATA AAC TGG GCT GTC TGG CAG GCG ATA AAC TAC ATT CAG TTG AGT    180
      181   CTG CAA GAC TGG GAG GAA CTG GGG TGA TAA GAA ATC TAT TCA CTG    225
 10   226   TCA AGG TTT ATT GAA GTC AAA ATG TCC AAA AAA ATC AGT GGC GGT    270
                                          M   S   K   K   I   S   G   G    8
      271   TCT GTG GTA GAG ATG CAA GGA GAT GAA ATG ACA CGA ATC ATT TGG    315
       9    S   V   V   E   M   Q   G   D   E   M   T   R   I   I   W     23
      316   GAA TTG ATT AAA GAG AAA CTC ATT TTT CCC TAC GTG GAA TTG GAT    360
 15    24    E   L   I   K   E   K   L   I   F   P   Y   V   E   L   D    38
      361   CTA CAT AGC TAT GAT TTA GGC ATA GAG AAT CGT GAT GCC ACC AAC    405
       39    L   H   S   Y   D   L   G   I   E   N   R   D   A   T   N    53
      406   GAC CAA GTC ACC AAG GAT GCT GCA GAA GCT ATA AAG AAG CAT AAT    450
       54    D   Q   V   T   K   D   A   A   E   A   I   K   K   H   N    68
 20   451   GTT GGC GTC AAA TGT GCC ACT ATC ACT CCT GAT GAG AAG AGG GTT    495
       69    V   G   V   K   C   A   T   I   T   P   D   E   K   R   V    83
      496   GAG GAG TTC AAG TTG AAA CAA ATG TGG AAA TCA CCA AAT GGC ACC    540
       84    E   E   F   K   L   K   Q   M   W   K   S   P   N   G   T    98
      541   ATA CGA AAT ATT CTG GGT GGC ACG GTC TTC AGA GAA GCC ATT ATC    585
 25    99    I   R   N   I   L   G   G   T   V   F   R   E   A   I   I    113
      586   TGC AAA AAT ATC CCC CGG CTT GTG AGT GGA TGG GTA AAA CCT ATC    630
      114   C   K   N   I   P   R   L   V   S   G   W   V   K   P   I    128
      631   ATC ATA GGT CGT CAT GCT TAT GGG GAT CAA TAC AGA GCA ACT GAT    675
      129   I   I   G   R   H   A   Y   G   D   Q   Y   R   A   T   D    143
 30   676   TTT GTT GTT CCT GGG CCT GGA AAA GTA GAG ATA ACC TAC ACA CCA    720
      144   F   V   V   P   G   P   G   K   V   E   I   T   Y   T   P    158
      721   AGT GAC GGA ACC CAA AAG GTG ACA TAC CTG GTA CAT AAC TTT GAA    765
      159   S   D   G   T   Q   K   V   T   Y   L   V   H   N   F   E    173
      766   GAA GGT GGT GGT GTT GCC ATG GGG ATG TAT AAT CAA GAT AAG TCA    810
 35   174   E   G   G   G   V   A   M   G   M   Y   N   Q   D   K   S    188
      811   ATT GAA GAT TTT GCA CAC AGT TCC TTC CAA ATG GCT CTG TCT AAG    855
      189   I   E   D   F   A   H   S   S   F   Q   M   A   L   S   K    203
      856   GGT TGG CCT TTG TAT CTG AGC ACC AAA AAC ACT ATT CTG AAG AAA    900
      204   G   W   P   L   Y   L   S   T   K   N   T   I   L   K   K    218
 40   901   TAT GAT GGG CGT TTT AAA GAC ATC TTT CAG GAG ATA TAT GAC AAG    945
      219   Y   D   G   R   F   K   D   I   F   Q   E   I   Y   D   K    233
      946   CAG TAC AAG TCC CAG TTT GAA GCT CAA AAG ATC TGG TAT GAG CAT    990
      234   Q   Y   K   S   Q   F   E   A   Q   K   I   W   Y   E   H    248
      991   AGG CTC ATC GAC GAC ATG GTG GCC CAA GCT ATG AAA TCA GAG GGA    1035
 45   249   R   L   I   D   D   M   V   A   Q   A   M   K   S   E   G    263
      1036  GGC TTC ATC TGG GCC TGT AAA AAC TAT GAT GGT GAC GTG CAG TCG    1080
      264   G   F   I   W   A   C   K   N   Y   D   G   D   V   Q   S    278
      1081  GAC TCT GTG GCC CAA GGG TAT GGC TCT CTC GGC ATG ATG ACC AGC    1125
      279   D   S   V   A   Q   G   Y   G   S   L   G   M   M   T   S    293
 50   1126  GTG CTG GTT TGT CCA GAT GGC AAG ACA GTA GAA GCA GAG GCT GCC    1170
      294   V   L   V   C   P   D   G   K   T   V   E   A   E   A   A    308
      1171  CAC GGG ACT GTA ACC CGT CAC TAC CGC ATG TAC CAG AAA GGA CAG    1215
      309   H   G   T   V   T   R   H   Y   R   M   Y   Q   K   G   Q    323
      1216  GAG ACG TCC ACC AAT CCC ATT GCT TCC ATT TTT GCC TGG ACC AGA    1260
 55   324   E   T   S   T   N   P   I   A   S   I   F   A   W   T   R    338
      1261  GGG TTA GCC CAC AGA GCA AAG CTT GAT AAC AAT AAA GAG CTT GCC    1305
      339   G   L   A   H   R   A   K   L   D   N   N   K   E   L   A    353
      1306  TTC TTT GCA AAT GCT TTG GAA GAA GTC TCT ATT GAG ACA ATT GAG    1350
      354   F   F   A   N   A   L   E   E   V   S   I   E   T   I   E    368
 60   1351  GCT GGC TTC ATG ACC AAG GAC TTG GCT GCT TGC ATT AAA GGT TTA    1395
      369   A   G   F   M   T   K   D   L   A   A   C   I   K   G   L    383
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```
     1396  CCC AAT GTG CAA CGT TCT GAC TAC TTG AAT ACA TTT GAG TTC ATG   1440
     384    P   N   V   Q   R   S   D   Y   L   N   T   F   E   F   M    398
     1441  GAT AAA CTT GGA GAA AAC TTG AAG ATC AAA CTA GCT CAG GCC AAA   1485
     399    D   K   L   G   E   N   L   K   I   K   L   A   Q   A   K    413
5    1486  CTT TAA GTT CAT ACC TGA GCT AAG AAG GAT AAT TGT CTT TTG GTA   1530
     414    L   *
     1531  ACT AGG TCT ACA GGT TTA CAT TTT TCT GTG TTA CAC TCA AGG ATA   1575
     1576  AAG GCA AAA TCA ATT TTG TAA TTT GTT TAG AAG CCA GAG TTT ATC   1620
     1621  TTT TCT ATA AGT TTA CAG CCT TTT TCT TAT ATA TAC AGT TAT TGC   1665
10   1666  CAC CTT TGT GAA CAT GGC AAG GGA CTT TTT TAC AAT TTT TAT TTT   1710
     1711  ATT TTC TAG TAC CAG CCT AGG AAT TCG TTA GTT ACT CAT TTG TAT   1755
     1756  TCA CTG TCA CTT TTT CTC ATG TTC TAA TTA TAA ATG ACC AAA ATC   1800
     1801  AAG ATT GCT CAA AAG GGT AAA TGA TAG CCA CAG TAT TGC TCC CTA   1845
     1846  AAA TAT GCA TAA AGT AGA AAT TCA CTG CCT TCC CCT CCT GTC CAT   1890
15   1891  GAC CTT GGG CAC AGG GAA GTT CTG GTG TCA TAG ATA TCC CGT TTT   1935
     1936  GTG AGG TAG AGC TGT GCA TTA AAC TTG CAC ATG ACT GGA ACG AAG   1980
     1981  TAG GAG TGC AAC TCA AAT GTG TTG AAG ATA CTG CAG TCA TTT TTG   2025
     2026  TAA AGA CCT TGC TGA ATG TTT CCA ATA GAC TAA ATA CTG TTT AGG   2070
     2071  CCG CAG GAG AGT TTG GAA TCC GGA ATA AAT ACT ACC TGG AGG TTT   2115
20   2116  GTC CTC TCC ATT TTT CTC TTT CTC CTC CTG GCC TGG CCT GAA TAT   2160
     2161  TAT ACT ACT CTA AAT AGC ATA TTT CAT CCA AGT GCA ATA ATG TAA   2205
     2206  GCT GAA TCT TTT TTG GAC TTC TGC TGG CCT GTT TTA TTT CTT TTA   2250
     2251  TAT AAA TGT GAT TTC TCA GAA ATT GAT ATT AAA CAC TAT CTT ATC   2295
     2296  TTC TCC     2301
```

Figure 2:

ORF of Isocitrate dehydrogenase 2 (NM_002168)

(nucleic acid sequence: SEQ ID NO:3; amino acid sequence: SEQ ID NO:4)

```
   1 ccagcgttagcccgcggccaggcagccgggaggagcggcgcgcgctcggacctctcccgc
  61 cctgctcgttcgctctccagcttgggatggccggctacctgcgggtcgtgcgctcgctct
   1                            M  A  G  Y  L  R  V  V  R  S  L
 121 gcagagcctcaggctcgcggccggcctgggcgccggcggccctgacagcccccacctcgc
  12 C  R  A  S  G  S  R  P  A  W  A  P  A  A  L  T  A  P  T  S
 181 aagagcagccgcggcgccactatgccgacaaaaggatcaaggtggcgaagcccgtggtgg
  32 Q  E  Q  P  R  R  H  Y  A  D  K  R  I  K  V  A  K  P  V  V
 241 agatggatggtgatgagatgacccgtattatctggcagttcatcaaggagaagctcatcc
  52 E  M  D  G  D  E  M  T  R  I  I  W  Q  F  I  K  E  K  L  I
 301 tgccccacgtggacatccagctaaagtattttgacctcgggctcccaaaccgtgaccaga
  72 L  P  H  V  D  I  Q  L  K  Y  F  D  L  G  L  P  N  R  D  Q
 361 ctgatgaccaggtcaccattgactctgcactggccacccagaagtacagtgtggctgtca
  92 T  D  D  Q  V  T  I  D  S  A  L  A  T  Q  K  Y  S  V  A  V
 421 agtgtgccaccatcacccctgatgaggcccgtgtggaagagttcaagctgaagaagatgt
 112 K  C  A  T  I  T  P  D  E  A  R  V  E  E  F  K  L  K  K  M
 481 ggaaaagtcccaatggaactatccggaacatcctggggggggactgtcttccgggagccca
 132 W  K  S  P  N  G  T  I  R  N  I  L  G  G  T  V  F  R  E  P
 541 tcatctgcaaaaacatcccacgcctagtccctggctggaccaagcccatcaccattggca
 152 I  I  C  K  N  I  P  R  L  V  P  G  W  T  K  P  I  T  I  G
 601 ggcacgcccatggcgaccagtacaaggccacagactttgtggcagaccgggccggcactt
 172 R  H  A  H  G  D  Q  Y  K  A  T  D  F  V  A  D  R  A  G  T
 661 tcaaaatggtcttcaccccaaaagatggcagtggtgtcaaggagtgggaagtgtacaact
 192 F  K  M  V  F  T  P  K  D  G  S  G  V  K  E  W  E  V  Y  N
 721 tccccgcaggcggcgtgggcatgggcatgtacaacaccgacgagtccatctcaggttttg
 212 F  P  A  G  G  V  G  M  G  M  Y  N  T  D  E  S  I  S  G  F
 781 cgcacagctgcttccagtatgccatccagaagaaatggccgctgtacatgagcaccaaga
 232 A  H  S  C  F  Q  Y  A  I  Q  K  K  W  P  L  Y  M  S  T  K
 841 acaccatactgaaagcctacgatgggcgtttcaaggacatcttccaggagatctttgaca
 252 N  T  I  L  K  A  Y  D  G  R  F  K  D  I  F  Q  E  I  F  D
 901 agcactataagaccgacttcgacaagaataagatctggtatgagcaccggctcattgatg
 272 K  H  Y  K  T  D  F  D  K  N  K  I  W  Y  E  H  R  L  I  D
 961 acatggtggctcaggtcctcaagtcttcggggtggctttgtgtgggcctgcaagaactatg
 292 D  M  V  A  Q  V  L  K  S  S  G  G  F  V  W  A  C  K  N  Y
1021 acggagatgtgcagtcagacatcctggcccaaggcttggcctcccttggcctgatgacgt
 312 D  G  D  V  Q  S  D  I  L  A  Q  G  F  G  S  L  G  L  M  T
1081 ccgtcctggtctgcccctgatgggaagacgattgaggctgaggccgctcatgggaccgtca
 332 S  V  L  V  C  P  D  G  K  T  I  E  A  E  A  H  G  T  V
1141 cccgccactatcgggagcaccagaagggccggcccaccagcaccaaccccatcgccagca
 352 T  R  H  Y  R  E  H  Q  K  G  R  P  T  S  T  N  P  I  A  S
1201 tctttgcctggacacgtggcctggagcaccggggggaagctggatgggaaccaagacctca
 372 I  F  A  W  T  R  G  L  E  H  R  G  K  L  D  G  N  Q  D  L
1261 tcaggtttgcccagatgctggagaaggtgtgcgtggagacggtggagagtggagccatga
 392 I  R  F  A  Q  M  L  E  K  V  C  V  E  T  V  E  S  G  A  M
1321 ccaaggacctggcgggctgcattcacggcctcagcaatgtgaagctgaacgagcacttcc
 412 T  K  D  L  A  G  C  I  H  G  L  S  N  V  K  L  N  E  H  F
1381 tgaacaccacggacttcctcgacaccatcaagagcaacctggacagagccctgggcaggc
 432 L  N  T  T  D  F  L  D  T  I  K  S  N  L  D  R  A  L  G  R
1441 agtagggggaggcgccacccatggctgcagtggaggggccagggctgagccggcgggtcc
 452 Q  *
1501 tcctgagcgcggcagagggtgagcctcacagcccctctctggaggcctttctaggggatg
1561 ttttttttataagccagatgttttttaaaagcatatgtgtgtttcccctcatggtgacgtga
1621 ggcaggagcagtgcgttttacctcagccagtcagtatgttttgcatactgtaatttatat
1681 tgcccttggaacacatggtgccatatttagctactaaaaagctcttcacaaaaaaaaaaa
```

Figure 3:

Isocitrate dehydrogenas   anti sense fragment

(SEQ ID NO: 5)

5

5' TGCTCTGTGGGCTAACCCTCTGGTCCAGGCAAAAATGGAAGCAATGGGATTGGTGGACGTCTCCTGT

CCTTTCTGGTACATGCGGTAGTGACGGGTTACAGTCCCGTGGGCAGCCTCTGCTTCTACCGTCTTGCCA

TCTGGACAAACCAGCACGCTGGTCATCATGCCGAGAGAGCCATACCCTTGGGCCACAGAGTCCGACTGC

ACGTCACCATCATAGTTTTTACAGGCCCAGATGAAGCCTCCCTCTGATCTCATAGCTGGGGCCACCATG

10 TCGTCGATGAGCCTATGCTCATACCAGATCTTTTGAGCTTCAAACTGGGACTTGTACTGCTTGTCATAT

ATCTCCTGAAAGATGTCTTTAAAACGCCCATCATATTTCTTCAGAATGGTGTTTTTGGTGCTCAGATAC

AAAGGCCAACCCTTAGACAGAGCCATTTGGAAGGAACTGTGTGCAAAATCTTCAATTGACTTATCTTGA

TTATACATCCCCATGACAACACCACCACCTTCTTCAAGTTATGTACCAGG' 3

Applicants: Paz Einat et al.
U.S. Serial No.: Not Yet Known
Filing Date: July 11, 2003
Title: ISOCITRATE DEHYDROGENASE AND
       USES THEREOF
4 of 12

Figure 4:

IDH siRNA sequence

(SEQ ID NO:6)

5   5′ AATCGTGATGCCACCAACGAC `3

Figure 5:

Alignment between Isocitrate dehydrogenase 1 (XM_055088) and AS fragment

```
5   ICD      1    GGCGGCGAAGCGGGGGCACGCCCTCGCACACGCAGAGATAAATTGTGCTCCCATGACCTT
    IRT-4C1   1    ------------------------------------------------------------

    ICD      61   TATTTGGAAAGTGCCTGCGGGCCTAAAATTGGCCTTTGTCCCACCGAGTACACTCAGCAC
    IRT-4C1   1    ------------------------------------------------------------
10
    ICD      121  TGTACTTTAAACCGGATAAACTGGGCTGTCTGGCAGGCGATAAACTACATTCAGTTGAGT
    IRT-4C1   1    ------------------------------------------------------------

    ICD      181  CTGCAAGACTGGGAGGAACTGGGGTGATAAGAAATCTATTCACTGTCAAGGTTTATTGAA
15  IRT-4C1   1    ------------------------------------------------------------

    ICD      241  GTCAAAATGTCCAAAAAAATCAGTGGCGGTTCTGTGGTAGAGATGCAAGGAGATGAAATG
    IRT-4C1   1    ------------------------------------------------------------
20  ICD      301  ACACGAATCATTTGGGAATTGATTAAAGAGAAACTCATTTTTCCCTACGTGGAATTGGAT
    IRT-4C1   1    ------------------------------------------------------------

    ICD      361  CTACATAGCTATGATTTAGGCATAGAGAATCGTGATGCCACCAACGACCAAGTCACCAAG
    IRT-4C1   1    ------------------------------------------------------------
25
    ICD      421  GATGCTGCAGAAGCTATAAAGAAGCATAATGTTGGCGTCAAATGTGCCACTATCACTCCT
    IRT-4C1   1    ------------------------------------------------------------

    ICD      481  GATGAGAAGAGGGTTGAGGAGTTCAAGTTGAAACAAATGTGGAAATCACCAAATGGCACC
30  IRT-4C1   1    ------------------------------------------------------------

    ICD      541  ATACGAAATATTCTGGGTGGCACGGTCTTCAGAGAAGCCATTATCTGCAAAAATATCCCC
    IRT-4C1   1    ------------------------------------------------------------

35  ICD      601  CGGCTTGTGAGTGGATGGGTAAAACCTATCATCATAGGTCGTCATGCTTATGGGGATCAA
    IRT-4C1   1    ------------------------------------------------------------

    ICD      661  TACAGAGCAACTGATTTTGTTGTTCCTGGGCCTGGAAAAGTAGAGATAACCTACACACCA
    IRT-4C1   1    ------------------------------------------------------------
40
    ICD      721  AGTGACGGAACCCAAAAGGTGACATACCTGGTACATAACTTTGAAGAAGGTGGTGGTGTT
    IRT-4C1   1    ------------------------CCTGGTACATAAC-TTGAAGAAGGTGGTGGTGTT

    ICD      781  GCCATGGGGATGTATAATCAAGATAAGTCAATTGAAGATTTTGCACACAGTTCCTTCCAA
45  IRT-4C1   34   GTCATGGGGATGTATAATCAAGATAAGTCAATTGAAGATTTTGCACACAGTTCCTTCCAA

    ICD      841  ATGGCTCTGTCTAAGGGGTTGGCCTTTGTATCTGAGCACCAAAAACACTATTCTGAAGAAA
    IRT-4C1   94   ATGGCTCTGTCTAAGGGGTTGGCCTTTGTATCTGAGCACCAAAAACACCATTCTGAAGAAA

50  ICD      901  TATGATGGGCGTTTTAAAGACATCTTTCAGGAGATATATGACAAGCAGTACAAGTCCCAG
    IRT-4C1   154  TATGATGGGCGTTTTAAAGACATCTTTCAGGAGATATATGACAAGCAGTACAAGTCCCAG

    ICD      961  TTTGAAGCTCAAAAGATCTGGTATGAGCATAGGCTCATCGACGACATGGTGGCCCAAGCT
    IRT-4C1   214  TTTGAAGCTCAAAAGATCTGGTATGAGCATAGGCTCATCGACGACATGGTGGCCCCAGCT
55
    ICD      1021 ATGAAATCAGAGGGAGGCTTCATCTGGGCCTGTAAAAACTATGATGGTGACGTGCAGTCG
    IRT-4C1   274  ATGAGATCAGAGGGAGGCTTCATCTGGGCCTGTAAAAACTATGATGGTGACGTGCAGTCG

    ICD      1081 GACTCTGTGGCCCAAGGGTATGGCTCTCTCGGCATGATGACCAGCGTGCTGGTTTGTCCA
60  IRT-4C1   334  GACTCTGTGGCCCAAGGGTATGGCTCTCTCGGCATGATGACCAGCGTGCTGGTTTGTCCA

    ICD      1141 GATGGCAAGACAGTAGAAGCAGAGGCTGCCCACGGGACTGTAACCCGTCACTACCGCATG
    IRT-4C1   394  GATGGCAAGACGGTAGAAGCAGAGGCTGCCCACGGGACTGTAACCCGTCACTACCGCATG

65  ICD      1201 TACCAGAAAGGACAGGAGACGTCCACCAATCCCATTGCTTCCATTTTTGCCTGGACCAGA
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```
IRT-4C1   454  TACCAGAAAGGACAGGAGACGTCCACCAATCCCATTGCTTCCATTTTTGCCTGGACCAGA

ICD      1261  GGGTTAGCCCACAGAGCAAAGCTTGATAACAATAAAGAGCTTGCCTTCTTTGCAAATGCT
IRT-4C1   514  GGGTTAGCCCACAGAGCA-------------------------------------------

ICD      1321  TTGGAAGAAGTCTCTATTGAGACAATTGAGGCTGGCTTCATGACCAAGGACTTGGCTGCT
IRT-4C1   531  ------------------------------------------------------------

ICD      1381  TGCATTAAAGGTTTACCCAATGTGCAACGTTCTGACTACTTGAATACATTTGAGTTCATG
IRT-4C1   531  ------------------------------------------------------------

ICD      1441  GATAAACTTGGAGAAAACTTGAAGATCAAACTAGCTCAGGCCAAACTTTAAGTTCATACC
IRT-4C1   531  ------------------------------------------------------------

ICD      1501  TGAGCTAAGAAGGATAATTGTCTTTTGGTAACTAGGTCTACAGGTTTACATTTTTCTGTG
IRT-4C1   531  ------------------------------------------------------------

ICD      1561  TTACACTCAAGGATAAAGGCAAAATCAATTTTGTAATTTGTTTAGAAGCCAGAGTTTATC
IRT-4C1   531  ------------------------------------------------------------

ICD      1621  TTTTCTATAAGTTTACAGCCTTTTTCTTATATATACAGTTATTGCCACCTTTGTGAACAT
IRT-4C1   531  ------------------------------------------------------------

ICD      1681  GGCAAGGGACTTTTTTACAATTTTTATTTTATTTTCTAGTACCAGCCTAGGAATTCGGTT
IRT-4C1   531  ------------------------------------------------------------

ICD      1741  AGTACTCATTTGTATTCACTGTCACTTTTTCTCATGTTCTAATTATAAATGACCAAAATC
IRT-4C1   531  ------------------------------------------------------------

ICD      1801  AAGATTGCTCAAAAGGGTAAATGATAGCCACAGTATTGCTCCCTAAAATATGCATAAAGT
IRT-4C1   531  ------------------------------------------------------------

ICD      1861  AGAAATTCACTGCCTTCCCCTCCTGTCCATGACCTTGGGCACAGGGAAGTTCTGGTGTCA
IRT-4C1   531  ------------------------------------------------------------

ICD      1921  TAGATATCCCGTTTTGTGAGGTAGAGCTGTGCATTAAACTTGCACATGACTGGAACGAAG
IRT-4C1   531  ------------------------------------------------------------

ICD      1981  TAGGAGTGCAACTCAAATGTGTTGAAGATACTGCAGTCATTTTTGTAAAGACCTTGCTGA
IRT-4C1   531  ------------------------------------------------------------

ICD      2041  ATGTTTCCAATAGACTAAATACTGTTTAGGCCGCAGGAGAGTTTGGAATCCGGAATAAAT
IRT-4C1   531  ------------------------------------------------------------

ICD      2101  ACTACCTGGAGGTTTGTCCTCTCCATTTTTCTCTTTCTCCTCCTGGCCTGGCCTGAATAT
IRT-4C1   531  ------------------------------------------------------------

ICD      2161  TATACTACTCTAAATAGCATATTTCATCCAAGTGCAATAATGTAAGCTGAATCTTTTTTG
IRT-4C1   531  ------------------------------------------------------------

ICD      2221  GACTTCTGCTGGCCTGTTTTATTTCTTTTATATAAATGTGATTTCTCAGAAATTGATATT
IRT-4C1   531  ------------------------------------------------------------

ICD      2281  AAACACTATCTTATCTTCTCCTG
IRT-4C1   531  -----------------------
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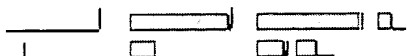
Figure 6
Alignment between IDH2 and IDH1 amino acid sequences

```
Score =   584 bits (1505), Expect = e-165
Identities = 281/397 (70%), Positives = 328/397 (81%); Gaps = 2/397
(0%)
```



```
IDH2:  50  VVEMDGDEMTRIIWQFIKEKLILPHVDIQLKYFDLGLPNRDQTDDQVTIDSALATQKYSV  109
           VVEM GDEMTRIIW+ IKEKLI P+V++ L  +DLG+ NRD T+DQVT D+A A +K++V
IDH1:  10  VVEMQGDEMTRIIWELIKEKLIFPYVELDLHSYDLGIENRDATNDQVTKDAAEAIKKHNV   69

IDH2: 110  AVKCATITPDEARVEEFKLKKMWKSPNGTIRNILGGTVFREPIICKNIPRLVPGWTKPIT  169
           VKCATITPDE RVEEFKLK+MWKSPNGTIRNILGGTVFRE IICKNIPRLV GW KPI
IDH1:  70  GVKCATITPDEKRVEEFKLKQMWKSPNGTIRNILGGTVFREAIICKNIPRLVSGWVKPII  129

IDH2: 170  IGRHAHGDQYKATDFVADRAGTFKMVFTPKDGSGVKEWEVYNFP-AGGVGMGMYNTDESI  228
           IGRHA+GDQY+ATDFV    G  ++ +TP DG+    + V+NF   GGV MGMYN D+SI
IDH1: 130  IGRHAYGDQYRATDFVVPGPGKVEITYTPSDGTQKVTYLVHNFEEGGGVAMGMYNQDKSI  189

IDH2: 229  SGFAHSCFQYAIQKKWPLYMSTKNTILKAYDGRFKDIFQEIFDKHYKTDFDKNKIWYEHR  288
                FAHS FQ A+ K WPLY+STKNTILK  YDGRFKDIFQEI+DK YK+ F+  KIWYEHR
IDH1: 190  EDFAHSSFQMALSKGWPLYLSTKNTILKKYDGRFKDIFQEIYDKQYKSQFEAQKIWYEHR  249

IDH2: 289  LIDDMVAQVLKSSGGFVWACKNYDGDVQSDILAQGFGSLGLMTSVLVCPDGKTIEAEAAH  348
           LIDDMVAQ +KS GGF+WACKNYDGDVQSD +AQG+GSLG+MTSVLVCPDGKT+EAEAAH
IDH1: 250  LIDDMVAQAMKSEGGFIWACKNYDGDVQSDSVAQGYGSLGMMTSVLVCPDGKTVEAEAAH  309

IDH2: 349  GTVTRHYREHQKGRPTSTNPIASIFAWTRGLEHRGKLDGNQDLIRFAQMLEKVCVETVES  408
           GTVTRHYR +QKG+ TSTNPIASIFAWTRGL HR KLD N++L  FA  LE+V +ET+E+
IDH1: 310  GTVTRHYRMYQKGQETSTNPIASIFAWTRGLAHRAKLDNNKELAFFANALEEVSIETIEA  369

IDH2: 409  GAMTKDLAGCIHGLSNVKLNEHFLNTTDFLDTIKSNL  445
           G MTKDLA CI GL NV+ ++ +LNT +F+D +  NL
IDH1: 370  GFMTKDLAACIKGLPNVQRSD-YLNTFEFMDKLGENL  405
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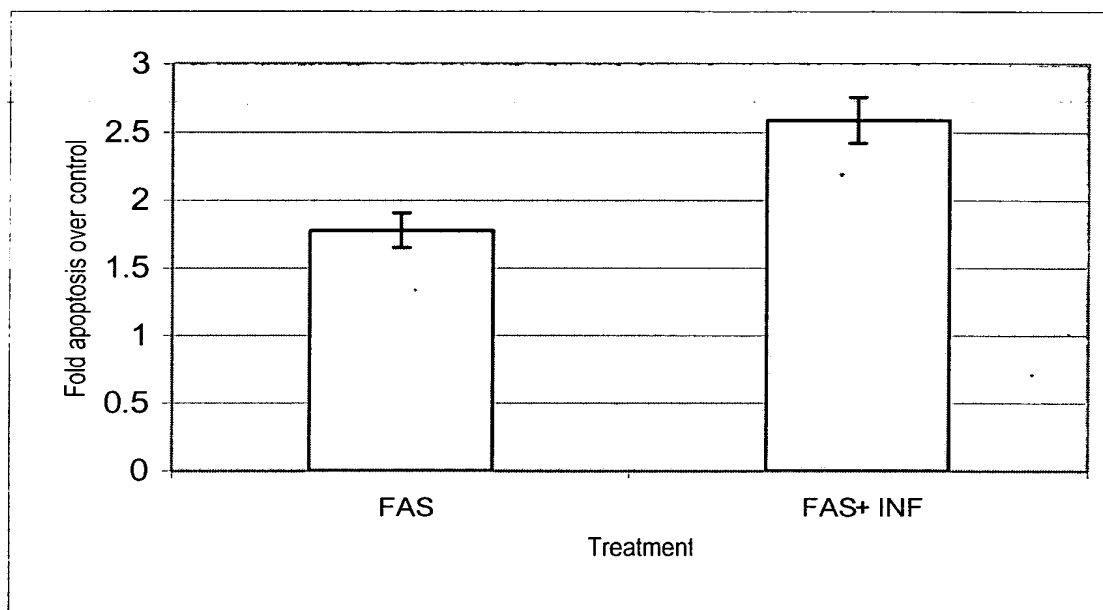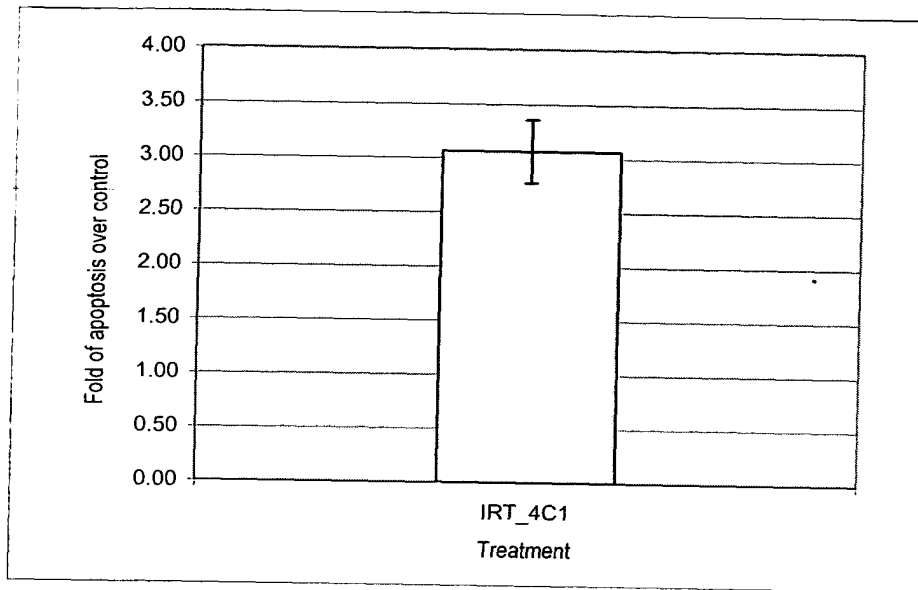
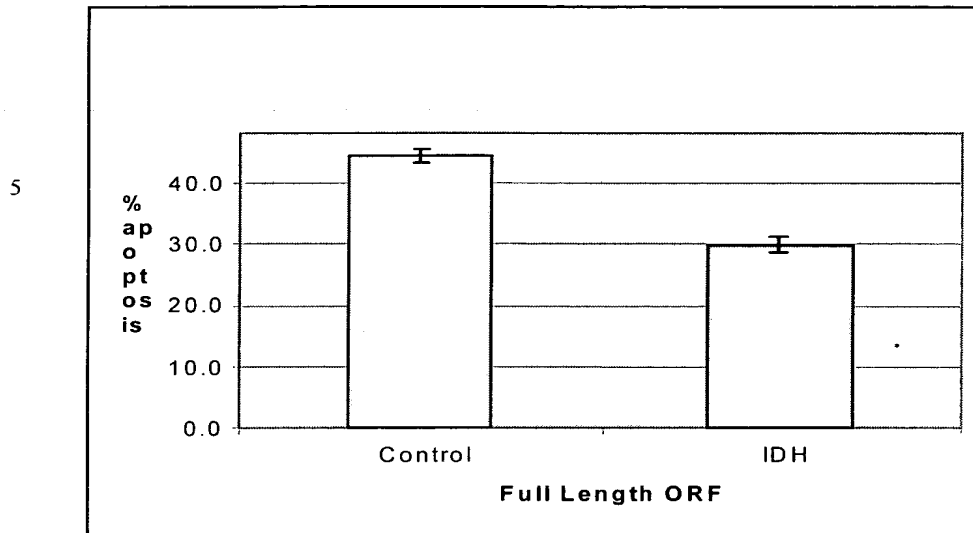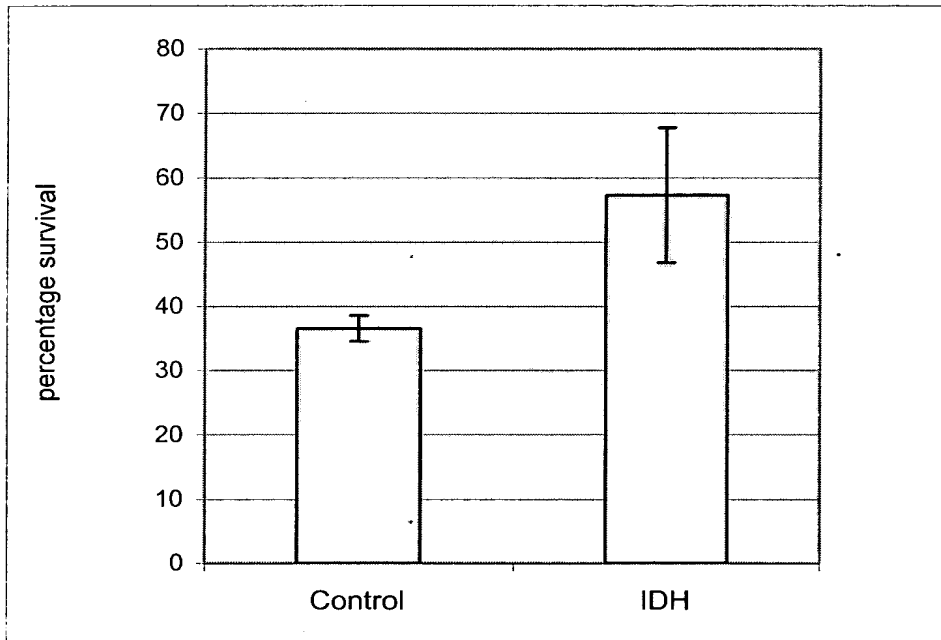## Figure 7

Figure 8

Figure 9

A) apoptosis protection

Full Length ORF

B) viability assay

Figure 10